



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/724,806	12/01/2003	Randy D. Blakely	VBLT:008USD1	3686

7590 08/09/2006

Steven L. Highlander, Esq.
FULBRIGHT & JAWORSKI L.L.P.
Suite 2400
600 Congress Avenue
Austin, TX 78701

EXAMINER

BUNNER, BRIDGET E

ART UNIT	PAPER NUMBER
----------	--------------

1647

DATE MAILED: 08/09/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/724,806

Applicant(s)

BLAKELY ET AL.

Examiner

Bridget E. Bunner

Art Unit

1647

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 09 June 2004.
- 2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 29-36 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 29-36 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 09 June 2004 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>3/5/04</u> . | 6) <input checked="" type="checkbox"/> Other: <u>Appendices A, B, C, D</u> |

DETAILED ACTION

Status of Application, Amendments and/or Claims

The amendment of 01 December 2003 has been entered in full. Claims 1-28 and 37-105 are cancelled.

Claims 29-36 are under consideration in the instant application.

Information Disclosure Statement

The information disclosure statement filed 05 March 2004 fails to comply with 37 CFR 1.98(a)(3) because it does not include a concise explanation of the relevance, as it is presently understood by the individual designated in 37 CFR 1.56(c) most knowledgeable about the content of the information, of each patent listed that is not in the English language (document DE 10009055). It has been placed in the application file, but the information referred to therein has not been considered.

Sequence Compliance

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). **Specifically, the sequences disclosed in Figure 2 and Figure 4 are not accompanied by the required reference to the relevant sequence identifiers.** This application fails to comply with the requirements of 37 CFR 1.821 through 1.825. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825).

Claim Objections

2. Claim 29 is objected to because of the following informalities:

Art Unit: 1647

2a. In claim 29, line 1 is missing the term “acid” after “amino”. Appropriate correction is required.

Specification

3. The disclosure is objected to because of the following informalities:

3a. Patent applications are referenced throughout the disclosure (for example, pg 136, line 22). The status of the applications must be updated.

3b. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code (See for example, pg 20, line 20; pg 25, line 17; pg 46, line 24). Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

3c. The Brief Description of Drawings for Figure 11 at pg 10-11 of the specification does not refer to Figures 11C or 11D.

3d. The Brief Description of Drawings for Figure 14 at pg 11 of the specification does not refer to Figures 14A and 14B.

3e. The reference cited at pg 3, line 10 (Apparsundaram 2001) needs to be updated as it is still listed as “in press”.

3f. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

The following title is suggested: “POLYNUCLEOTIDE ENCODING A MURINE CHOLINE TRANSPORTER”.

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 29-36 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO: 4 and for an isolated polynucleotide comprising the nucleic acid sequence as set forth in SEQ ID NO: 3, does not reasonably provide enablement for an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence essentially as set forth in SEQ ID NO: 4 or for an isolated polynucleotide comprising the nucleic acid sequence essentially as set forth in SEQ ID NO: 3. The specification is also not enabling for a purified and isolated polynucleotide comprising a sequence identical or complementary to between 10 and 100 contiguous nucleotides of SEQ ID NO: 3. The specification is also not enabling for a recombinant vector or recombinant host cell comprising a DNA segment encoding any isolated murine choline transporter. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

It is noted that the phrases “comprising/having ...essentially as set forth in SEQ ID NO:”, “an isolated choline transporter” (for example, claim 34), and “(c)DNA segment” as recited in the claims, are broadly interpreted by the Examiner as reading upon: (i) nucleic acid variants of SEQ ID NO: 3 with any number of deletions, substitutions, or additions and (ii) protein variants of SEQ ID NO: 4 with any number of deletions, substitutions, or additions.

Specifically, the claims are directed to an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence essentially as set forth in SEQ ID NO: 4 and an isolated polynucleotide comprising the nucleic acid sequence essentially as set forth in SEQ ID NO: 3. The claims also recite a purified and isolated polynucleotide comprising a sequence identical or complementary to between 10 and 100 contiguous nucleotides of SEQ ID NO: 3. The claims recite that the polynucleotide is comprising in a vector. The claims also recite a recombinant vector comprising a DNA segment encoding a mouse choline transporter polypeptide under the control of a promoter.

The specification of the instant application teaches that nucleic acid variants may be any length and that "a DNA segment encoding CHT refers to a DNA segment that contains wild-type, polymorphic or mutant CHT coding sequences yet is isolated away from, or purified free from, total mammalian genomic DNA. Included within the term "DNA segment," are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like" (pg 23, lines 7-12; pg 30; pg 42). The specification teaches only teaches a murine CHT polynucleotide and polypeptide of SEQ ID NO: 3 and SEQ ID NO: 4, respectively. The specification does not teach any variants, fragments, or derivatives of the nucleic acid sequence of SEQ ID NO: 3. The specification does not teach any variants, fragments, or derivatives of a polynucleotide that encodes the polypeptide of SEQ ID NO: 4. The specification also does not teach all possible DNA segments that encode an isolated murine choline transporter. Further, the specification does not teach functional or structural characteristics of the polynucleotide variants, fragments, or derivatives in the context of a cell or organism.

The problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex. While it is known that many amino acid substitutions are generally possible in any given protein the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions in the DNA and amino acid sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. These or other regions may also be critical determinants of antigenicity. These regions can tolerate only relatively conservative substitutions or no substitutions (see Wells, 1990, *Biochemistry* 29:8509-8517; Ngo et al., 1994, *The Protein Folding Problem and Tertiary Structure Prediction*, pp. 492-495). For example, Okuda et al. (*J Biol Chem* 277(47): 45315-45322, 2002) teach that a single amino acid change from an isoleucine to a valine at amino acid position 89 in the human choline transporter causes a 40-50% decrease in choline uptake as compared with wild-type (pg 45317, col 2, ¶ 2; pg 45319, col 1-2; Figure 3, Table II, Figure 6B, C). Okuda et al. also demonstrate that introduction of an isoleucine in place of valine at corresponding amino acid position 90 in the *C. elegans* ortholog (CHO-1) also causes a 40% decrease in choline uptake with unaltered affinity for choline (pg 45319, col 2 through pg 45320, col 1; Figure 6D, E).

However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the DNA and protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made

Art Unit: 1647

in these positions. Although the specification outlines art-recognized procedures for producing and screening for active muteins, this is not adequate guidance as to the nature of active derivatives that may be constructed, but is merely an invitation to the artisan to use the current invention as a starting point for further experimentation. Even if an active or binding site were identified in the specification, they may not be sufficient, as the ordinary artisan would immediately recognize that an active or binding site must assume the proper three-dimensional configuration to be active, which conformation is dependent upon surrounding residues; therefore substitution of non-essential residues can often destroy activity. The art recognizes that function cannot be predicted from structure alone (Bork, 2000, *Genome Research* 10:398-400; Skolnick et al., 2000, *Trends in Biotech.* 18(1):34-39, especially p. 36 at Box 2; Doerks et al., 1998, *Trends in Genetics* 14:248-250; Smith et al., 1997, *Nature Biotechnology* 15:1222-1223; Brenner, 1999, *Trends in Genetics* 15:132-133; Bork et al., 1996, *Trends in Genetics* 12:425-427).

Additionally, the Examiner has interpreted claims 89-91 as reading on isolated host cells, as well as host cells in the context of a multicellular, transgenic organism and host cells intended for gene therapy. The specification of the instant application teaches that CHT gene product can be expressed in transgenic animals (for example pg 7, lines 28-29; pg 8, lines 1-8). However, there are no methods or working examples disclosed in the instant application whereby a multicellular animal with the incorporated mCHT gene of SEQ ID NO: 3 is demonstrated to express the mCHT polypeptide. The unpredictability of the art is *very high* with regards to making transgenic animals. For example, Wang et al. (*Nuc. Acids Res.* 27: 4609-4618, 1999; pg 4617) surveyed gene expression in transgenic animals and found in each experimental animal

Art Unit: 1647

with a single "knock-in" gene, multiple changes in genes and protein products, often many of which were unrelated to the original gene. Likewise, Kaufman et al (Blood 94: 3178-3184, 1999) found transgene expression levels in their transfected animals varied from "full" (9 %) to "intermediate" to "none" due to factors such as "vector poisoning" and spontaneous structural rearrangements (pg 3180, col 1, 2nd full paragraph; pg 3182-3183). Therefore, , it would have required undue experimentation for the skilled artisan to have made any and all transgenic non-human animals according to the instant invention.

The specification also discloses that nucleic acids encoding the mCHT polypeptide can be used for gene therapy (pg 3, line 22). However, the specification does not teach any methods or working examples that indicate a mCHT nucleic acid is introduced and expressed in a cell for therapeutic purposes. The disclosure in the specification is merely an invitation to the artisan to use the current invention as a starting point for further experimentation. For example, the specification does not teach what type of vector would introduce the mCHT nucleic acid into the cell or in what quantity and duration. Relevant literature teaches that since 1990, about 3500 patients have been treated via gene therapy and although some evidence of gene transfer has been seen, it has generally been inadequate for a meaningful clinical response (Phillips, A., J Pharm Pharmacology 53: 1169-1174, 2001; abstract). Additionally, the major challenge to gene therapy is to deliver DNA to the target tissues and to transport it to the cell nucleus to enable the required protein to be expressed (Phillips, A.; pg 1170, ¶ 1). Phillips also states that the problem with gene therapy is two-fold: 1) a system must designed to deliver DNA to a specific target and to prevent degradation within the body, and 2) an expression system must be built into the DNA construct to allow the target cell to express the protein at therapeutic levels for the desired length

Art Unit: 1647

of time (pg 1170, ¶ 1). Therefore, undue experimentation would be required of the skilled artisan to introduce and express a mCHT nucleic acid into the cell of an organism. Additionally, gene therapy is unpredictable and complex wherein one skilled in the art may not necessarily be able to introduce and express a mCHT nucleic acid in the cell of an organism or be able to produce a mCHT protein in that cell. (Please note that this issue could be overcome by amending the claims to recite, for example, "An isolated host cell...").

Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen the same for activity, and to generate a transgenic animal expressing the mCHT protein and to introduce and express a mCHT nucleic acid in a cell of an organism for therapy; the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity and how to introduce a mCHT nucleic acid in the cell of an organism to be able produce that mCHT; the absence of working examples directed to same; the complex nature of the invention; the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function and the unpredictability of making transgenic animals and of transferring genes into an organism's cells; and the breadth of the claims which fail to recite any structural or functional limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

5. Claims 29-36 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant

Art Unit: 1647

art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Specifically, the claims are directed to an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence essentially as set forth in SEQ ID NO: 4 and an isolated polynucleotide comprising the nucleic acid sequence essentially as set forth in SEQ ID NO: 3. The claims also recite a purified and isolated polynucleotide comprising a sequence identical or complementary to between 10 and 100 contiguous nucleotides of SEQ ID NO: 3. The claims recite that the polynucleotide is comprising in a vector. The claims also recite a recombinant vector comprising a DNA segment encoding a mouse choline transporter polypeptide under the control of a promoter.

It is noted that the phrases “comprising/having ... essentially as set forth in SEQ ID NO:”, “an isolated choline transporter” (for example, claim 34), and “(c)DNA segment” as recited in the claims, are broadly interpreted by the Examiner as reading upon: (i) nucleic acid variants of SEQ ID NO: 3 with any number of deletions, substitutions, or additions and (ii) protein variants of SEQ ID NO: 4 with any number of deletions, substitutions, or additions.

The specification of the instant application teaches that nucleic acid variants may be any length and that “a DNA segment encoding CHT refers to a DNA segment that contains wild-type, polymorphic or mutant CHT coding sequences yet is isolated away from, or purified free from, total mammalian genomic DNA. Included within the term “DNA segment,” are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like” (pg 23, lines 7-12; pg 30; pg 42). However, the claims do not require that the nucleic acid or polypeptide possess any particular

Art Unit: 1647

biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of nucleic acid molecules.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, there is not even identification of any particular portion of the nucleic acid structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus. Additionally, the description of one mCHT polynucleotide species (SEQ ID NO: 3) and one mCHT polypeptide species (SEQ ID NO: 4) is not adequate written description of an entire genus of functionally equivalent polynucleotides and polypeptides which incorporate all variants, fragments, and derivatives of SEQ ID NO: 3 and SEQ ID NO: 4.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states that “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the ‘written description’ inquiry, *whatever is now claimed*” (See page 1117). The specification does not “clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed” (See *Vas-Cath* at page 1116).

With the exception of the sequences referred to above, the skilled artisan cannot envision the detailed chemical structure of the encompassed polynucleotides, and therefore conception is

Art Unit: 1647

not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The nucleic acid itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only an isolated nucleic acid molecule consisting of the nucleic acid sequence of SEQ ID NO:3 and a nucleic acid molecule which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO:4, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 29-34 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Art Unit: 1647

7. Claims 29-34 are rejected as being indefinite because the claims fail to define the metes and bounds of the phrase “comprising/having...essentially as set forth in SEQ ID NO:”. For example, it is not clear if this language is open or closed or what polynucleotides/polypeptides are encompassed.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

8. Claims 29-34 and 36 are rejected under 35 U.S.C. 102(b) as being anticipated by Okuda et al. (Nat Neurosci 3(2): 120-125, 2000; Genbank Accession No. AB030947). It is noted that the phrase “comprising/having ...essentially as set forth in SEQ ID NO:”, as recited in the claims, is broadly interpreted by the Examiner as reading upon: (i) nucleic acid variants of SEQ ID NO: 3 with any number of deletions, substitutions, or additions and (ii) protein variants of SEQ ID NO: 4 with any number of deletions, substitutions, or additions.

Okuda et al. teach an isolated “CHT1” polynucleotide that is 92.7% identical to the nucleic acid sequence of SEQ ID NO: 3 of the instant application (see sequence alignment attached to the instant Office Action as Appendix A). The CHT1 polynucleotide of Okuda et al. comprises a nucleic acid sequence that is identical to at least 134 contiguous nucleotides of SEQ ID NO: 3 of the instant application (see nucleic acids 1418-1551 of Okuda et al. and nucleic

Art Unit: 1647

acids 1195-1328 of SEQ ID NO:3 of the instant application). Okuda et al. also disclose that the CHT1 polynucleotide encodes a choline transporter polypeptide (see sequence alignment attached to the instant Office Action as Appendix B; see Figure 2a of Okuda et al.) Okuda et al. teach that the CHT1 cDNA is isolated and subcloned into the pcDNA3.1+ vector, which contains a cytomegalovirus immediate early (CMV) promoter/enhancer (pg 124, 2nd full paragraph). Okuda et al. disclose transfecting COS7 cells with the CHT1/pcDNA3.1+ vector (pg 124, Figure 5).

9. Claims 29-36 are rejected under 35 U.S.C. 102(a) as being anticipated by Haga et al. (WO 0116315; 08 March 2001; see also pg 24-25 of CA 2382464 (Canadian translation of WO 0116315)).

Haga et al. teach an isolated murine polynucleotide that is 99.3% identical to the nucleic acid sequence of SEQ ID NO: 3 of the instant application (see sequence alignment attached to the instant Office Action as Appendix C; see also SEQ ID NO: 7 of Haga et al.). The CHT1 polynucleotide of Haga et al. comprises a nucleic acid sequence that is identical to over 100 contiguous nucleotides of SEQ ID NO: 3 of the instant application (see nucleic acids 356-1733 of Haga et al. and nucleic acids 356-1733 of SEQ ID NO:3 of the instant application). Haga et al. also disclose that the CHT1 polynucleotide encodes a choline transporter polypeptide (see sequence alignment attached to the instant Office Action as Appendix D; see SEQ ID NO: 8 of Haga et al.) Haga et al. teach that the gene encoding the mCHT protein may be introduced into a host cell by a number of different methods (pg 22, lines 13-26). Haga et al. teach that vectors

Art Unit: 1647

may used as an expression system to express the protein in a host cell and that the vectors may contain a regulatory sequence that acts as a promoter (pg 23, lines 7-17).

Art Unit: 1647

Conclusion

No claims are allowable.

The art made of record and not relied upon is considered pertinent to applicant's disclosure:

Wu et al. (U.S. Patent 6,500,643) (SEQ ID NO : 1 of Wu et al. is 79.1% identical to SEQ ID NO: 3 of the instant application)

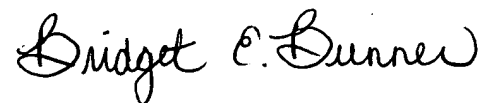
Invitrogen 2001 catalog, pg 155 (pcDNA vectors)

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Bridget E. Bunner whose telephone number is (571) 272-0881. The examiner can normally be reached on 8:30-4:30 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Brenda Brumback can be reached on (571) 272-0961. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

BEB
Art Unit 1647
04 August 2006


**BRIDGET BUNNER
PATENT EXAMINER**

Appendix A

Db 1441 ACTCTCTCCATGGTACCTCATCTTTTACCAACATTTGTGTTTCTATCTTCAAGTAT 1500
Qy 1501 CTATTTGAAGTGAACCTTCCCTCCAAATAGATGATTTGATGCTGTTGCGCAGG 1560
Db 1501 CTATTTGAAGTGAACCTTCCCTCCAAATAGATGATTTGATGCTGTTGCGCAGG 1560
Qy 1561 CACAGTGAAGAGACATGAGCAAGACCATCTTCTAGTCAAGAAATGAAATTAAT 1620
Db 1561 CACAGTGAAGAGACATGAGCAAGACCATCTTCTAGTCAAGAAATGAAATTAAT 1620
Qy 1621 GAACCTGCACCTGTGAACCTCGCAGACCTTAACCTTCACTTCACTTCAACAAATAG 1680
Db 1621 GAACCTGCACCTGTGAACCTCGCAGACCTTAACCTTCACTTCACTTCAACAAATAG 1680
Qy 1681 GAGGCTCTCTTGTATGTTGTTCCAGTCCGAGGGGCTGCGGACTGAAGATAATTTCAA 1740
Db 1681 GAGGCTCTCTTGTATGTTGTTCCAGTCCGAGGGGCTGCGGACTGAAGATAATTTCAA 1740
Qy 1741 TGA 1743
Db 1741 TGA 1743

RESULT 9
AB030947
LOCUS
DEFINITION Rattus norvegicus mRNA for high-affinity choline transporter CHT1, complete cds.
ACCESSION AB030947
VERSION AB030947.1 GI:6863033
KEYWORDS choline transporter; high-affinity choline transporter CHT1.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (sites)
Okuda, T., Haga, T., Kanai, Y., Endou, H., Ishihara, T. and Katsura, I.
Identification and characterization of the high-affinity choline transporter
Nat. Neurosci. 3 (2), 120-125 (2000)
PUBMED 10649566
REFERENCE 2 (bases 1 to 4904)
Okuda, T.
AUTHORS Direct Submission
JOURNAL Submitted (09-AUG-1999) Takashi Okuda, University of Tokyo, Faculty of Medicine, Department of Neurochemistry, Hongo 7-3-1, Bunkyo-ku 113-0033, Japan (E-mail:okuda@n.u-tokyo.ac.jp, Tel: +81-3-5841-3560, Fax: +81-3-3814-8154)
COMMENT Sequence updated (11-Jan-2000).
FEATURES
source
1..4904
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/clone="CHT1"
/tissue_type="spinal.cord"
/clone_lib="rat spinal cord cDNA library"
/dev_stage="adult"
224..1966
/codon_start=1
/product="high-affinity choline transporter CHT1"
/protein_id="BAA30484.1"
/db_xref="GI:6863034"
/translation="MPHFVEGLVAIILFYLLIFLVGIWAAMKTNKNABERSAIV
GGRIIGLVGGTWTATVWGGYINGTAEAVYGGGLAWAQAIPYLSLILGLFF
AKPMSKGYTMDLPFOQIYKRMGGLFIPALMGEMFWAAIFESALGARTSLIIVD
VNIISVVSALIALITLVGLSVYADVQVLFGLWISVFPALSHAVTDIGT
AVHAKYOSPMILTESVEVYTWLNDLMLGGIPWQAYFORVLSSSSATVAQLSEL
AATGCLVWALPAICIGAGTADWNQAYGFPDPKTEADMLPIVLQICPVYISF
FGLGAVSAAMSSADSSILSSAMFARNIYQLSPRONASDKEIIVWNRITVVFEGSA

ORIGIN
Query Match 92.7%; Score 1616.6; DB 6; Length 4904;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 1664; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
DSSPESGSGEDNQLQ"
1 ATGCTTTTCCATGTGGAGGACTAGTATCTTCTTCTACCTCTTATTTCTG 60
224 ATGCTTTTCCATGTAGAAGGACTAGTATCTTCTTCTACCTCTTATTTCTG 283
61 GTTGGAAATATGGCTGTCATGAAACCAAAACAGCGGCAACCCAGAGAGCGAGTAA 120
284 GTTGGAAATATGGCTGTCATGAAACCAAAACAGCGGCAACCCAGAGAGCGAGTAA 343
121 GCATCATATGTCGGGGCGGTGACATTTGTTTGTGTTGTTGTTGTTTACCATGACGCC 180
344 GCATCATATGTCGGGGCGGTGACATTTGTTTGTGTTGTTGTTTACCATGACGCC 403
181 ACCTGGGTTGGAGGAGCTACATCAATGGGACAGAGAGAGAGAGAGAGAGTGT 240
404 ACCTGGGTTGGAGGAGCTACATCAATGGGACAGAGAGAGAGAGAGAGTGT 463
241 GGTCTAGCTTGGGCTCATGACCCATTTGATATTTCTGAGTCTAAATTTAGTGGTCTG 300
464 GGTCTAGCTTGGGCTCAGGACCCATTTGATATTTCTGAGTCTGATTTAGTGGTCTG 523
301 TTTTTCGGAACCTATGCGTTTCAAGGGATATGTGATATTTAGTACCCATTTCAACAG 360
524 TTTTTCGGAACCTATGCGTTTCAAGGGATATGTGATATTTAGTACCCATTTCAACAG 583
361 ATCTATGGAAGCGCATGGGTGGCTCTCTTCTATCTCTGCTGATGGGAGAGATGTC 420
584 ATCTATGGAAGCGCATGGGTGGCTCTCTTCTATCTCTGCTGATGGGAGAGATGTC 643
421 TGGGCTCAGCAATTTTCTCTGATTAAGGGCCACCATCAGCGTGATCATTTAGTGGAT 480
644 TGGGCTCAGCAATTTTCTCTGATTAAGGGCTACCATCAGCGTGATCATTTAGTGGAT 703
481 GTGAACATATCGGTCAATTTCTCTGCTATTCGCACTCATTTATATCCCTAGTGGTGG 540
704 GTGAACATATCGGTCAATTTCTCTGCTATTCGCACTCATTTATATCCCTAGTGGTGG 763
541 CTCTACTCTGTGGCATATCTGATTTGTCAGTATTTCTGATTTTATAGGACTGTGG 600
764 CTCTACTCTGTGGCATATCTGATTTGTCAGTATTTCTGATTTTATAGGACTGTGG 823
601 ATCAGTGTCTCTTTGCTCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 660
824 ATCAGTGTCTCTTTGCTCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 883
661 CATGCTAAATACAGAGTCTCTGCTGGGAAACCAATGAATCAGTTGAAGTCTACACCTGG 720
884 CATGCTAAATACAGAGTCTCTGCTGGGAAACCAATGAATCAGTTGAAGTCTACACCTGG 943
721 CTGATTAATTTCTGTTTATGATGTCGGGTGGAATCCCATGGGAGAGCTTCTCAGAGG 780
944 CTGATTAATTTCTGTTTATGATGTCGGGTGGAATCCCATGGGAGAGCTTCTCAGAGG 1003
781 GTCTCTCTCTTCTCTCAGGACCTATGCTCAGTACTGCTCTCTCTCTCTCTCTCTCTCTCT 840
1004 GTCTCTCTCTCTCTCAGGACCTATGCTCAGTACTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1063
841 TGCTGTGTGATGGCTCTACCCGCCATATGATAGGAGCTATTTGAGGCTTCCACAGACTGG 900
1064 TGCTGTGTGATGGCTCTACCCGCCATATGATAGGAGCTATTTGAGGCTTCCACAGACTGG 1123
901 AACAGAGTCTGCTACGGGTTTCCAGATCCCAAGACTHAGGAGGAGAGAGATGATCTC 960
1124 AACCAAACTGCATATGGGTTTCCAGATCCCAAGACTHAGGAGGAGAGAGATGATCTC 1183

Appendix A (cont.)

QY	961	CGAGTCGTTCTCGAGTACCTCTGCGGCTGTGTACATCTCCTCTTTGGGCTTGGTCTGTT	1020
* Db	1184	CGGATTTGTTCTACAGTACCTCTGCGGCTGTGTACATTTCTTCTTTGGGCTTGGTCTGTT	1243
QY	1021	TCAGCTGCTGTCATGTCCTCAGCTGATCTGTCCTCATCTCTGTGCGGAGTTCTATGTTTGTCT	1080
Db	1244	TTTGCTGCTGTGTCATGTCCTCGGCTGACTCATCTCATCTTATCAGCAAGTTCCATGTTTGTCT	1303
QY	1081	CGGAATATCTACCAAGCTTTCTTTTCAGACAAATGTCATCAGACAAAGGAAATGTTGTGGGTC	1140
Db	1304	CGGAATATCTACCAAGCTTTCTTTTCAGACAAATGTCATCAGACAAAGGAAATGTTGTGGGTC	1363
QY	1141	ATGAGGATCATGTGCTGTTGTGTTGCGAGCATCTGCAACAGGCCATGGGTTTGTCTGACGCAAG	1200
Db	1364	ATGAGGATCATGTGTTGTTGTTTGGAGCATCTGCAACAGGCCATGGGTTTGTCTGACGCAAG	1423
QY	1201	ACTGTGATGGGCTCTGCTGCTCTGAGCTCTGACGTTGTTGTTCTACATCATCTTCTCCACAG	1260
Db	1424	ACTGTGATGGGCTCTGCTGCTCTGAGCTCTGACGTTGTTGTTCTACATCATCTTCTCCACAG	1483
QY	1261	CTGCTCTGTGTACTTTTCATCAAAAGGAACCAACACTTTATGGGCAGTTGCTGGGTATATT	1320
Db	1484	CTGCTCTGTGTACTTTTCATCAAAAGGAACCAACACTTTATGGGCAGTTGCTGGGTATATT	1543
QY	1321	TTTCGACTATTCCTGAGAAATTATCGGAGGAGGCCATATCTATCTTGCAGGCCCTTAAATC	1380
Db	1544	TTTCGACTATTCCTGAGAAATTATCGGAGGAGGCCATATCTATCTTGCAGGCCCTTAAATC	1603
QY	1381	TTCTACCCCTGGTTATTACTCTGACAGAAATGGTATATACAATCAGAGGTTCCCATTTAAA	1440
Db	1604	TTCTACCCCTGGTTATTACCCTGACAGAAATGGTATATACAATCAGAGGTTCCCATTTAAA	1663
QY	1441	ACTCTCTCCATGGTTACTCTCAITTTTACCAACATTTGTTTCTTATCTAGCCAGTAT	1500
Db	1664	ACTCTCTCCATGGTTACTCTCAITTTTACCAACATTTGTTTCTTATCTAGCCAGTAT	1723
QY	1501	CTATTTTGAAGTGGAACTTGGCTTCCAAATTAGATGTATTTGATGCTGTTGTCGCAAGG	1560
Db	1724	CTATTTTGAAGTGGAACTTGGCTTCCAAATTAGATGTATTTGATGCTGTTGTCGCAAGG	1783
QY	1561	CACAGTGAAGAGAAATGGACAGACCAATTCATGTCAGAAATGAAATATCAATTTAAT	1620
Db	1784	CACAGTGAAGAGAAATGGACAGACCAATTCATGTCAGAAATGAAATATCAATTTAAT	1843
QY	1621	GAAC TTGCACTGTGAAA CTTGGCAGAGCCCTAACCCCTCAGTTCAACTTTTACCAATAAG	1680
Db	1844	GAAC TTGCACTGTGAAA CTTGGCAGAGCCCTAACCCCTCAGTTCAACTTTTACCAATAAG	1903
QY	1681	GAGGCCCTCTTCATGTTGATTTCCAGTCCGGAGGGGCTGCGGATGGAAGATATTTTCAA	1740
Db	1904	GAGGCTCTCTTGATGTTGATTTCCAGTCCAGAGGGATCTGGGACTGAAGATAACTTTCAA	1963
QY	1741	TGA 1743	
Db	1964	TGA 1966	

RESULT 10
AR268949
LOCUS
DEFINITION
AR268949
ACCESSION
AR268949
VERSION
AR268949.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
UNIVERSITY

Sequence 1 from patent US 6500643.
1743 bp
DNA
linear
US 6500643-A 1
GI:29699686
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1743)
Wu, D.-H., Gu, Y., Millard, W.J. and He, Y.-J.
Human high affinity choline transporter
Patent: US 6500643-A 1
31-DEC-2002;
University of Florida; Gainesville, FL

PAT 10-APR-2003

FEATURES					
	Location/Qualifiers				
..source	1. .1743				
	/organism="unknown"				
	/mol_type="genomic DNA"				
ORIGIN					
Query Match	79.1%	Score 1378.2;	DB 2;	Length 1743;	
Best Local Similarity	86.9%;	Pred. No. 0;			
Matches 1515; Conservative	0;	Mismatches 228;	Indels	0;	Gaps 0
QY	1	ATGCCCTTCCATGCTGGAGGACTGTAGCTATTATCCTCTCTCTACCTCCTTATATTTCTG	60		
Db	1	ATGGCTTTTCATGTGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGGCTG	60		
QY	61	GTTCGAATATGGCTGCATGGAAAAACAACACGCGCAACCCAGAGAGCGCAGTGAA	120		
Db	61	GTTCGAATATGGCTGCCTGGAGAACCAAACAGTGGCGCGCAGAAGACGCGAGGAA	120		
QY	121	GCCATCATAGTCGGGGCGGTGACATNTGGTTTGTGTGGTGTGTTTACCATCACAGCC	180		
Db	121	GCCATCATAGTTGGTGGCGGAGATATGGTTTATTTGTGTGGTGTGATTTACCATCAGCT	180		
QY	181	AACCTGGTTGGAGGAGGCTACATAATGGGACAGACAGACAGTGTATGGGCCAGGTGT	240		
Db	181	AACCTGGTGGAGGAGGTATCAATGGCCACAGCTGAAGCAGTTTTATGTAACAGGTTAT	240		
QY	241	GGCTTAGCTTGGGCTCATGCAACCAATGGGAATTTCTCTGAGTCTAATTTTAGTGTTCTG	300		
Db	241	GGCCTTAGCTTGGGCTCAGGCACCAATTTGATATTTCTTCTAGTCTGATTTTAGTGTTCTG	300		
QY	301	TTTTTGGAAACCTATGCGTTCCAMGGGATATGTACTATGTTAGACCCATTTCAAACAG	360		
Db	301	TTCTTTGAAAACCTATGCGTTCCAGGGGTATGTGACCAATTTAGACCCGTTTCAGCAA	360		
QY	361	ATCTATGGAAGCCATGGGTGGCTGCTCTCTTATCCCTGCACTGATGGGAGAGATGTTT	420		
Db	361	ATCTATGGAACCCATGGGGGGAAGTCTCTGTTTATTTCTGCACTGATGGGAGAAATGTTT	420		
QY	421	TGGCTGCAGCAATTTTCTATGCAATTAGGGGCCACCATCAGCGTGTATCTGATGTGGAT	480		
Db	421	TGGGCTGCAGCAATTTTCTGCTTTTGGGAGCCACCATCAGCGTGTATCTGATGTGGAT	480		
QY	481	GTGAACATATCGGTCTATGTCTCTGCACTCATGTGCCATTTCTTATACCTTAGTGGGTGG	540		
Db	481	ATGCACATTTCTGTATCATCTCTGCACTCATGTGCCACTCTGTACACACTGTTGGGAGG	540		
QY	541	CTCTACTCTGTGCATATCTGATGTTGTCAGCTATTCTGCATTTTATAGACTGTGG	600		
Db	541	CTCTATTCTGTGGGCTACACTGATGTGTTGAGCTCTTTTGCAATTTTGTAGGGTGTGG	600		
QY	601	ATCAGTGTGCTTTTGGCCCTGTGCATCTCTGAGTCACCGACATCGGATTTACACGCTGG	660		
Db	601	ATCAGGTTCCCTTTTGCATTGTGCATCTCTGAGTCGAGACATCGGGTTTCACTGCTGTG	660		
QY	661	CATGCTAATATACAGAGTCCCTGGCTGGGAAACAATGAATCAGTTTGAAGTCTACACCTGG	720		
Db	661	CATGCAAAATACAAAGCCGTGGCTGGGAACTGTGTGACTCATCTGAAGTCTACTCTTGG	720		
QY	721	CTTGATAATTTTCTGTTATTTGATGCTGGGTGGAATCCCATGGCAAGCCCTACTTCCAGAGG	780		
Db	721	CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGGCAAGCTACTTTTCAGAGG	780		
QY	781	GTCCCTCTTTCATCTTCAGCCACCTATGCTCAGGTACTGTCTCTCTGGCAGCTTTTGGG	840		
Db	781	GTCTCTCTTCTTCTTCAGCCACCTATGCTCAAGTGTGCTCTCTCTGGCAGCTTTTCGGG	840		
QY	841	TGCTGTGATGGCTCTACCGCCCATATGCAATAGAGCTATTGGAGCTTCCACAGACTGG	900		
Db	841	TGCTGTGATGGCCATCCAGCCATATCTCATTTGGGGCAATTTGAGGCTTCCACAGACTGG	900		
QY	901	AACCAAGACTCGCCTACGGGTATCCAGATCCCAAGACTAAGGAGNAGCAGATGATTCTC	960		
QY	901	NACCAAGCTGCATATGGGCTTCAGATCCCAAGACTACAGAGGAGCAGATGATTCTA	960		

FEATURES
source

Location/Qualifiers
1. .4904
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/clone="CHT1"
/issue_type="spinal cord"
/clone_lib="rat spinal cord cDNA library"
/dev_stage="adult"
224. .1966
CDS
/codon_start=1
/product="high-affinity choline transporter CHT1"
/protein_id="BA990484.1"
/db_xref="GI:6863034"
/translation="MPFHVEGLVAIILFYLLIFLVGIWAAWTKNGNAERSEAILV
GGRDILLVGGFTMTATVGGGYINGTAEAVYGGGLAWAQAPIGYSLIILGLFF
AKPMRSKGVYVWMLDPQOITYGKMGGLLFI PALMGEMFWAAAI FSAIGATISVIDV
VNISVLSALIALTYLTVGLGVAVATDVVOLFPI FGLWISVPFALSHPAVTDIGTF
AHAKYQSPWLGHTIESVEVYTWLDNFLLMLGGIPQVAYFORVLSSSSAYAOVLSF
AFPGULMALPAICIGAIGATDNWQNTAYGFDPDKTEADMLPIVLQHLPCVPYISF
FGLGAVSAAMSSADSIILSASSMFARNIYQLSFRQNASDKEIWMNRITVFPVGA
TAMALLTKTVYGLWYLSDLVYIIIPQLLCVLFIKGTNTYGAAGYIFGLFLRTG
EPYLYQLPIFYPGYVDKNGIYNORPPKLTSMWTSFFNTI CVSYLAKLYFESGLIF
PKLIDFADVSRHSEENMDKXILVRNENIKLNELAPVKPQSLTSLSTFTNKEALLDV
DPSFEGSGTEDNLQ"

ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 4904
Score: 2956.00 Matches: 572
Percent Similarity: 99.3% Conservative: 4
Best Local Similarity: 98.6% Mismatches: 4
Query Match: 98.8% Indels: 0
DB: 6 Gaps: 0

US-10-724-806-4 (1-580) x AB030947 (1-4904)

Qy	1	MetProPheHisValGluGlyLeuValAlaIleLeuPheTyrLeuLeuIlePheLeu	20
Db	224	ATGCCTTTCCATGTAGAGGACCTAGTAGGCATTATCCTGTTCTACCTCTTATATTTCTG	283
Qy	21	ValGlyIleTrpAlaIleTrpLysThrLysAsnSerGlyAsnProGluGluAsgSerGlu	40
Db	284	GTTGGAAATATGGCGTGCATCGAAACCAAAACAGCGGTAATGAGAAAGAACCGCAGCGAA	343
Qy	41	AlaIleIleValGlyGlyArgAspIleGlyLeuLeuValGlyGlyPheThrMetThrAla	60
Db	344	GCCATCATAGTTGGGGCCGAGACATTTGGTTGTTGGTGGTGTATACCATCACAGCC	403
Qy	61	ThrTrpValGlyGlyGlyTyrIleAsnGlyThrAlaGluAlaValTyrGlyProGlyCys	80
Db	404	ACCTGGGTTGGAGAGGTTACATCAACGGGACAGCTGAAGCAGTTTATGGCCAGGTTGT	463
Qy	81	GlyLeuAlaTrpAlaHisAlaProIleGlyTyrSerLeuSerLeuIleLeuGlyGlyLeu	100
Db	464	GGCTAGCTAGTTGGGCTCAGGCACCCATTGGGATATTCTCTGAGTCGATTTTAGGTGGCCGTG	523
Qy	101	PhePheAlaLysProMetArgSerLysGlyTyrValThrMetLeuAspPropheLysGln	120
Db	524	TTTTTTTGCAAAACCTATCGCTTCCAGGGGATATGTGACTATGTTAGACCCGTTTCAACAG	583
Qy	121	IleTyrGlyLysArgMetGlyGlyLeuLeuPheIleProAlaLeuMetGlyGluMetPhe	140
Db	584	ATCTATGGAAGCGCATGGGTGGGCTGCTGTTTCATCCCTGCACATGATGGGAGAGATGTC	643
Qy	141	TrpAlaAlaAlaIlePheSerAlaLeuGlyAlaThrIleSerValIleIleAspValAsp	160
Db	644	TGGGCTGCAGCAATTTTCTCTGATTAGGGGCTACCATCAGCGGTAATCATTTGATGTGGAT	703
Qy	161	ValAsnIleSerValIleValSerAlaLeuIleAlaIleLeuTyrThrLeuValGlyGly	180
Db	704	GTGAACATATCGGTCATGTGCTCGGACTCATTTGCCATTTCTTATACCTCGGGGAGGG	763

181 LeuTyrSerValAlaTyrThrAspValValGlnLeuPheCysValPheIleGlyLeuTyrP 200
 764 CTCTACTCTGTGGCATATACATGTTGTACAGCTATCTGCAATTTATAGATTGTGG 823
 201 IleSerValProPheAlaLeuSerHisProAlaValThrAspIleGlyPheThrAlaVal 220
 824 ATCAGTGTCCCATTTGCCCTGTACATCTCGAGTCACCGACATTTGATTCAGTCTGTG 883
 221 HisAlaLysTyrClnSerProTyrPheGlyThrIleGlySerValGluValTyrThrTTP 240
 884 CATGTAATAATACAGAGTCCCTGGCTGGGAACATTTGAATGATGTTGAAGCTTACACCTGG 943
 241 LeuAspAsnPheLeuLeuMetLeuGlyGlyIleProTyrGlnAlaTyrPheGlnArg 260
 944 CTTGATAATTTCTGTTGTTGATGCTGGTGGATACCATGCGAAGCTTCTCCAGAGG 1003
 261 ValLeuSerSerSerAlaThrTyrAlaGlnValLeuSerPheLeuAlaPheGly 280
 1004 GTCCCTCTCTTCATCGTCAGCGACCTATGCTCAGGTGCTGCTCTCTCTGTCAGCTTTTGGG 1063
 281 CysLeuValMetAlaLeuProAlaIleCysIleGlyAlaIleGlyAlaSerThrAspTTP 300
 1064 TGCCTGGTGTGATGGCTCTACCGACCATTTTGCATTTGGGGCCATTGGAGCTTCCACAGACTGG 1123
 301 AsnGlnThrAlaTyrGlyTyrProAspProLysThrLysGluGluAlaAspMetIleLeu 320
 1124 AACCAACTGCAATGTTGTTTCAGATCCCAAGACCAAGAGGAGGACAGACATGATTCTC 1183
 321 ProIleValLeuGlnTyrLeuCysProValTyrIleSerPhePheGlyLeuGlyAlaVal 340
 1184 CCGATTGTTCTACAGTACCTCTGCCCTGTGTACATTTCTCTTTGGGCTGGTGTCTGT 1243
 341 SerAlaAlaValMetSerSerAlaAspSerSerIleLeuSerAlaSerSerMetPheAla 360
 1244 TCTGTCTGTCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
 361 ArgAsnIleTyrGlnLeuSerPheArgGlnAsnAlaSerAspLysGluIleValTTPVal 380
 1304 CGGATAATCTACAGCTTTCTTCTTTCAGCAAAATGATCATCAGACAGGAATTTGTGGTCT 1363
 381 MetArgIleThrValLeuValPheGlyAlaSerAlaThrAlaMetAlaLeuLeuThrLys 400
 1364 ATGAGGATCACTGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGTCCTTGTCTCAGGAG 1423
 401 ThrValTyrGlyLeuTyrIleLeuSerSerAspLeuValTyrIleIleIlePheProGln 420
 1424 ACTGTGTATGGCTCTGGTACCTGAGCTCTGACCTTGTCTACATCATCATCTTCCACAG 1483
 421 LeuLeuCysValLeuPheIleLysGlyThrAsnThrTyrGlyAlaValAlaGlyTyrIle 440
 1484 CTGCTCTGTGTACTTCTCATCAAGAACCAACATTTATGGGGCAGTTGCTGTTATATT 1543
 441 PheGlyLeuPheLeuArgIleThrGlyGlyGluProTyrIleLeuGlnProLeuIle 460
 1544 TTTGGACTTTTCTGAGAAATACCGAGGAGAGCCATATCTATCTTGGAGCCCTTAATC 1603
 461 PheTyrProGlyTyrTyrSerAspLysAsnGlyIleTyrAsnGlnArgPheProPheLys 480
 1604 TTCTACCCCTGGTATTACCTGCAAGAATGGTATATACAAATCAGAGGTTTCCCATTTAAA 1663
 481 ThrLeuSerMetValThrSerPhePheThrAsnIleCysValSerTyrLeuAlaLysTyr 500
 1664 ACTCTCTCATGGTTACTCATTTCTTACCAACATTTGTGTTTCTTATCTAGCCAAAGTAT 1723
 501 LeuPheGluSerGlyThrLeuProProLysLeuAspValPheAspAlaValValAlaArg 520
 1724 CTATTTGAAAGTGAACCTTGCCTCCAAAATTAGATATATTTCATGCTGTGTCTCAAGG 1783
 521 HisSerGluAsnMetAspLysThrIleLeuValArgAsnGlnAsnIleLysLeuAsn 540
 1784 CACAGTGAAGAGAACATGGACAAGACCAATTTCTAGTCAGAAATGAAACATCAAAATTAAT 1843

541 GluLeuAlaProValLysProArgGlnSerLeuThrLeuSerSerThrPheThrAsnLys 560
 1844 GAACTTGACCTGTAAAGCCTCGACAGAGCTTACCCCTCAGTTCACTTCCACCAATAAA 1903
 561 GluAlaLeuLeuAspValAspSerSerProGluGlySerGlyThrGluAspAsnLeuGln 580
 1904 GAGGCTCTCTTGTGTTGATTCAGTCCAGAGGATCTGGAGTCTGAAGATAACTTACAA 1963

RESULT 10
 LOCUS BD012719 1743 bp DNA linear PAT 02-AUG-2002
 DEFINITION High-affinity choline transporter.
 ACCESSION BD012719
 VERSION BD012719.1 GI:22092908
 KEYWORDS WO 0116315-A/3.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 1 (bases 1 to 1743)
 Haga, T. and Okuda, T.
 High-affinity choline transporter
 Patent: WO 0116315-A 3 08-MAR-2001;
 JAPAN SCIENCE AND TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA
 COMMENT
 OS Homo sapiens (human)
 PN WO 0116315-A/3
 PD 08-MAR-2001
 PF 18-AUG-2000 WO 2000JP005545
 PR 27-AUG-1999 JP 99P 240542, 27-DEC-1999 JP 99P 368991 PI
 TATSUYA HAGA, TAKASHI OKUDA
 PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC
 A61K38/17,
 PC A61K45/00, A61P25/28, G01N33/53, A01K67/027
 CC
 FH Key Location/Qualifiers
 FT CDS (1)..(1743)
 1..1743
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 0 Length: 1743
 Score: 2795.00 Matches: 537
 Percent Similarity: 96.6% Conservative: 23
 Best Local Similarity: 92.6% Mismatches: 20
 Query Match: 93.4% Indels: 0
 DB: 2 Gaps: 0
 US-10-724-806-4 (1-580) x BD012719 (1-1743)

QY 1 MetProPheHisValGluGlyLeuValAlaIleIleLeuPheTyrIleLeuLeuPheLeu 20
 Db 1 ATGGCTTCCATGTGGAAGGACTGATAGTATCATCTCGTGTCTTACCTTCTAAATTTTGTG 60
 QY 21 ValGlyIleTTPAlaAlaTTPLysThrLysAsnSerGlyAsnProGluGluArgSerGlu 40
 Db 61 GTTGGATATGGCTGGCTTGGAGAACCAAAACAGTGGCGGCGGAGAGCGGCGGAA 120
 QY 41 AlaIleIleValGlyGlyArgAspIleGlyLeuLeuValGlyGlyPheThrMetThrAla 60
 Db 121 GCATCATAGTTGGTGGCCGAGATATTGTTTATTGTTGGTGGATTACCATGACAGCT 180
 QY 61 ThrTTPValGlyGlyGlyTyrIleAsnGlyThrAlaGluAlaValTyrGlyProGlyCys 80
 Db 181 ACCTGGGTGGAGGAGGTTATATCAATGCGACAGCTGAAGCAGTTTATGTACAGGTTAT 240
 QY 81 GlyLeuAlaTTPAlaHisAlaProIleGlyTyrSerLeuSerLeuLeuGlyGlyLeu 100
 Db 241 GGCTAGCTTGGGCTCAGGCCCAATTTGATATTCTCTTAGTCTGATTTTAGTGGCTG 300

2

RESULT: 3
 BD012720
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 Mus musculus (house mouse)
 Mus musculus
 Hagi, T. and Okuda, T.
 1 (bases 1 to 1743)
 High-affinity choline transporter
 Patent: WO 0116315-A 4 08-MAR-2001;
 JAPAN SCIENCE AND TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA
 OS Mus musculus (mouse)
 PN WO 0116315-A/4
 PD 08-MAR-2001
 PF 18-AUG-2000 WO 2000JP005545
 PR 27-AUG-1999 JP 99P 240642, 27-DEC-1999 JP 99P 368991 PI
 TATSUYA HAGA, TAKASHI OKUDA
 PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC
 A61K38/17,
 PC A61K45/00, A61P25/28, G01N33/53, A01K67/027
 CC
 FH Key Location/Qualifiers
 FT CDS (1)..(1743).
 Location/Qualifiers
 1..1743
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 FEATURES
 source
 Query Match 99.3%; Score 1730.2; DB 2; Length 1743;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1735; Conservative 0; Mismatches 8; Indels 0; Gaps 0
 QY 1 ATGCCTTTCCATGTGGAGGACTGGTAGCTATTCTCTTCTACCTCCTTATATTTCTG 60
 Db 1 ATGCTTTCCAGTAGAGGACTGGTAGCTATTCTCTTCTACCTCCTTATATTTCTG 60
 QY 61 GTTGGAAATATGGGTGCGATGGAAACCAAAAACAGCGGCCACCCAGAGAGCGCATGAA 120
 Db 61 GTTGGAAATATGGGTGCGATGGAAACCAAAAACAGCGGCCACCCAGAGAGCATGAA 120
 QY 121 GCCATCATAGTCGGGGCCGTGACATGGTTGTTGTTGGTTTACCATGACAGCC 180
 Db 121 GCCATCATAGTCGGGGCCGTGACATGGTTGTTGTTGGTTTACCATGACAGCC 180
 QY 181 ACCTGGGTGGAGGAGGCTACATCAATGGGACAGAGCAAGTGTATGGGCCAGGTTGT 240
 Db 181 ACCTGGGTGGAGGAGGCTACATCAATGGGACAGAGCAAGTGTATGGGCCAGGTTGT 240
 QY 241 GGTCTAGCTTGGGCTATGCAACCAATGGATATCTCTGAGTCTAATTTTAGTGCTG 300
 Db 241 GGTCTAGCTTGGGCTATGCAACCAATGGATATCTCTGAGTCTAATTTTAGTGCTG 300
 QY 301 TTTTTCGGAACCTATCGGTTCCAGGGATGTGACTATGTAGACCCATTCAACACAG 360
 Db 301 TTTTTCGGAACCTATCGGTTCCAGGGATGTGACTATGTAGACCCATTCAACACAG 360
 QY 361 ATCTATGAAACGCGATGGGTGGGCTGCTTTTCATCCCTGCATGATGGAGAGATGTT 420
 Db 361 ATCTATGAAACGCGATGGGTGGGCTGCTTTTCATCCCTGCATGATGGAGAGATGTT 420
 QY 421 TGGGCTGACGCAATTTTCTCTGCATAGGGGCCCAATCAGTCGTCATTCATGTTGGAT 480
 Db 421 TGGGCTGACGCAATTTTCTCTGCATAGGGGCCCAATCAGTCGTCATTCATGTTGGAT 480

Appendix D

Db 387 ATCTATGAAAGCGCATGGTGGCTGCTCTTTCATCCCTGCATGATGGAGAGATGTTTC 449
 QY 141 TTPAlaAlaAlaIlePheSerAlaLeuGlyAlaThrIleSerValIleIleAspValAsp 760
 Db 447 TGGGCTGCAAGCAATTTTCTCTGCAATAGGGGCCACCATCAGCTGATCATGATGGAG 506
 QY 161 ValAsnIleSerValIleValSerAlaLeuIleAlaIleLeuTyrThrLeuValGlyGly 180
 Db 507 GTGAACATATCGTCAATGCTCTGCACTCATGTCCTATTTTATACCTTAGTGGTGG 566
 QY 181 LeuTyrSerValAlaTyrThrAspValValGlnLeuPheCysIlePheIleGlyLeuTyr 200
 Db 567 CTCCTACTCTGTGCATATATGATGTGTCCAGCTATCTGCATTTTATATAGACTGTGG 626
 QY 201 IleSerValProPheAlaLeuSerHisProAlaValThrAspIleGlyPheThrAlaVal 220
 Db 627 ATCAGTGTCCCTTTTGGCTGTGCATCTGTGAGTCAACGACATCGGATTCACAGCTGTG 686
 QY 221 HisAlaLysTyrGlnSerProTyrLeuGlyThrIleGluSerValGluValTyrThrTyr 240
 Db 687 CATGCTAATATACAGAGTCCCTGGCTGGGAACCATGGAATCATTTGAAGTCTACACCTGG 746
 QY 241 LeuAspAsnPheLeuLeuLeuMetLeuGlyGlyIleProTyrGlnAlaTyrPheGlnArg 260
 Db 747 CTTGATAATTTCTGTATTGATGTGTGGTGGAAATCCCAAGGCAAGCTTCTCCAGAGG 806
 QY 261 ValLeuSerSerSerSerAlaThrTyrAlaGlnValLeuSerPheLeuAlaIlePheGly 280
 Db 807 GTCCCTCTCTCATCTCAGCCACCTATGCTCAGTACTGCTCTCTCTGCGACCTTTTGGG 866
 QY 281 CysLeuValMetAlaLeuProAlaIleCysIleGlyAlaIleGlyAlaSerThrAspTyr 300
 Db 867 TGCCTGGTGTGCTCTACCGCCATATGCATAGAGGCTATTGGAGCTTCCACAGACTGG 926
 QY 301 AsnGlnThrAlaTyrGlyTyrProAspPheThrLysGluGluAlaAspMetIleLeu 320
 Db 927 AACCAAGACTGCCTACCGGGTATCCAGATCCCAAGACTAAGAGAGAAAGACATGATTTCT 986
 QY 321 ProIleValLeuGlnTyrLeuCysProValTyrIleSerPhePheGlyLeuGlyAlaVal 340
 Db 987 CGATCGTCTCGAGTACCTCTGCTGATGATACCTCTCTCTTGGGCTTGGTGTCTGT 1046
 QY 341 SerAlaAlaValMetSerSerPheAspSerSerIleLeuSerAlaSerSerMetPheAla 360
 Db 1047 TCAGTGTGTGTCTATGCTCAGTCACTGCTGCTCATCTGCTGCGAGTCTCTATGTTGCT 1106
 QY 361 ArgAsnIleTyrGlnLeuSerPheArgGlnAsnAlaSerAspGlyGluIleValTyrVal 380
 Db 1107 CGGAATATCTACAGCTTTCTCTCAGACAAATGCAATGCAACAGAAATTTGTGGGTCT 1166
 QY 381 MetArgIleThrValLeuValPheGlyAlaSerAlaThrAlaMetAlaLeuLeuThrLys 400
 Db 1167 ATGAGATCATGCTGCTGTGTGTCGAGCATCTGCAACAGCCATGGCTTGTGTCAGAG 1226
 QY 401 ThrValTyrGlyLeuTyrThrLeuSerSerAspLeuValTyrIleIleIlePheProGln 420
 Db 1227 ACTGTGTATGGCTCTGGTACCTGAGCTGAGCTGACCTGCTACATCATCTCTCCACAG 1286
 QY 421 LeuLeuCysValLeuPheIleLysGlyThrAsnThrTyrGlyAlaValAlaGlyTyrIle 440
 Db 1287 CTGCTCAGTGTACTCTTCAAGAAACCAACACTATGAGGCGAGTGTGCTGTTATATT 1346
 QY 441 PheGlyLeuPheLeuArgIleThrGlyGluProTyrLeuTyrLeuGlnProLeuIle 460
 Db 1347 TTTGAGCTATTCTGAGAAATTAATCTGAGAGAGCCATATCATATCTTGAGCCCTTAATC 1406
 QY 461 PheTyrProGlyTyrTyrSerAspLysAsnGlyIleTyrAsnGlnArgPheProPheLys 480
 Db 1407 TTTTACCTGGTTATTACTCTGACAAGAAATGATATATACATCATCAGAGTTCCTCATTA 1466
 QY 481 ThrLeuSerMetValThrSerPheThrAsnIleCysValSerTyrLeuAlaLysTyr 500
 Db 1467 ACTCTCTCCATGGTTACCTCATCTTTTACCAACATTTGTGTTTCTTATCTAGCCAAATAT 1526

QY 501 LeuPheGluSerGlyThrLeuProLysLeuAspValPheAspAlaValValAlaArg 520
 Db 1527 CTAATTGAAGTGGAACTTGCCTCCAAATATAGATGTATTGAAGCTGTGTCGCAAGG 1586
 QY 521 HisSerGluGluAsnMetAspLysThrIleLeuValAsnGluAsnIleLysLeuAsn 540
 Db 1587 CACAGTGAAGAGACATGACAAAGCACTTCTGTCAGAAATGAATAATCAATTAAT 1646
 QY 541 GluLeuAlaProValLysProArgGlnSerLeuThrLeuSerSerThrPheThrAsnLys 560
 Db 1647 GAACCTGCACCTGTGAAACCTTGGCAGAGCCCTAACCTCAGTTCACCTTCCACCAATAG 1706
 QY 561 GluAlaLeuLeuAspValAspSerSerProGluGlySerGlyThrGluAspAsnLeuGln 580
 Db 1707 GAGGCCCTCTCTGATGTGTTGATTCAGTCCGAGGGGCTGCGAGCTGAAGATAACTTACAA 1766

RESULT 3

BD012720 1743 bp DNA linear PAT 02-AUG-2002
 Locus High-affinity choline transporter.

BD012720

ACCESSION BD012720

VERSION BD012720.1 GI:22092909

KEYWORDS WO 0116315-A/4.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Haga, T. and Okuda, T.

TITLE High-affinity choline transporter

JOURNAL Patent: WO 0116315-A 4 08-MAR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA

COMMENT OS Mus musculus (mouse)

PN WO 0116315-A/4

PD 08-MAR-2001

PF 18-AUG-2000 WO 2000JP005545

PR 27-AUG-1999 JP 99P 240642, 27-DEC-1999 JP 99P 368991 PI

PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC

A61K38/17, A61K45/00, A61P25/28, G01N33/53, A01K67/027

CC

PH

FT

Key Location/Qualifiers

1. 1743 (1) (1743).

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 0

Score: 2968.00

Percent Similarity: 99.5%

Best Local Similarity: 99.3%

Query Match: 99.2%

DB: 2

Length: 1743

Matches: 576

Conservative: 1

Mismatches: 3

Indels: 0

Gaps: 0

US-10-724-806-4 (1-580) x BD012720 (1-1743)

QY 1 MetProPheHisValGluGlyLeuValAlaIleIleLeuPheTyrLeuLeuIlePheLeu 20

Db 1 ATGTCTTTCCACGTAGAAGGACTGGTAGCTATTATCTCTTCTACCTCTTATATTCTG 60

QY 21 ValGlyIleTyrPalaAlaTyrLysThrLysAsnSerGlyAsnProGluGluArgSerGlu 40

Db 61 GTTGGAAATATGGCTGCTGATGAAACCAAAACAGCGGCAACCCAGAGACGACGTGA 120

QY 41 AlaIleIleValGlyGlyArgAspIleGlyLeuValGlyGlyPheThrMetThrAla 60

Db 121 GCCATCATAGTCGGGGCGGTGACATTTGGTTGGTGGTTTATCCATGACAGCC 180
 *Qy 61 ThrTrpValGlyGlyGlyThrIleAsnGlyThrAlaGluAlaValTyrGlyProGlyCys 80
 Db 181 ACCTGGGTGGAGAGGCTACATCAATGGGACAGCAGAGAGTGTATGGCCAGTTGT 240
 Qy 81 GlyLeuAlaTrpAlaHisAlaProIleGlyTyrSerLeuSerLeuLeuLeuGlyGlyLeu 100
 Db 241 GGTCTAGTGGCTCAGGCACCCATTCGATATTCTCTGAGTCTAAATTTAGGTGGTCTG 300
 Qy 101 PhePheAlaLysProMetArgSerLysGlyTyrValThrMetLeuAspProPheLysGln 120
 Db 301 TTTTITGCGAAACCTATCGTTTCCAGGGATATGTGACTATGTATAGACCCATTTCAACAG 360
 Qy 121 IleTyrGlyLysArgMetGlyGlyLeuLeuPheIleProAlaLeuMetGlyGluMetPhe 140
 Db 361 ATCTATGGAAGCGCATGGGTGGGTCTCTTCATCCCTGCACTGATGGAGAGATGTTTC 420
 Qy 141 TrpAlaAlaAlaIlePheSerAlaLeuGlyAlaThrIleSerValIleIleAspValAsp 160
 Db 421 TGGGCTGCAGCAATTTCTCTGCAATTAGGGCCACCATCAGCGTGATCATTTGATGGAT 480
 Qy 161 ValAsnIleSerValIleValSerAlaLeuIleAlaIleLeuTyrThrIleValGlyGly 180
 Db 481 GTGAACATATCGGTCTCTGCACTCATTTGCCATTTCTTTATACCTAGTGGGTGGG 540
 Qy 181 LeuTyrSerValAlaTyrThrAspValValGlnLeuPheCysIlePheIleGlyLeuTrp 200
 Db 541 CTCTACTCTGGGCATATCTGATGTGTCAGTATTTCTGCATTTTATAGACTGTGG 600
 Qy 201 IleSerValProPheAlaLeuSerHisProAlaValThrAspIleGlyPheThrAlaVal 220
 Db 601 ATCAGTGTCCCTTTTGGCTGTGCATCTCGAGTCACGACATCGGATTCACAGCTGTG 660
 Qy 221 HisAlaLysTyrGlnSerProTrpLeuGlyThrIleGluSerValGluValTyrThrTrp 240
 Db 661 CATGCTAAATACACAGAGTCCCTGGTGGGAACCAATGAAATGAACTGTAAGCTTACACCTGG 720
 Qy 241 LeuAspAsnPheLeuLeuMetLeuGlyGlyIleProTrpGlnAlaTyrPheGlnArg 260
 Db 721 CTTGATAATTTTCTGTATTGATGCTGGGTGGAAATCCCATGGCAAGCCTTCTCCAGAGG 780
 Qy 261 ValLeuSerSerSerAlaThrTyrAlaGlnValLeuSerPheLeuAlaAlaPheGly 280
 Db 781 GTCTCTCTTCTATCTCACCACCATGCTCAGTACTCTCTCTCTCTGTCAGCTTTTGGG 840
 Qy 281 CysLeuValMetAlaLeuProAlaIleCysIleGlyAlaIleGlyAlaSerThrAspTrp 300
 Db 841 TGCCTGGTGTATGGCTCTACCCGCGCATATGATAGGAGCTATTGGAGCTTCCACAGACTGG 900
 Qy 301 AsnGlnThrAlaTyrGlyTyrProAspProLysThrLysGluAlaAlaAspMetIleLeu 320
 Db 901 AAACAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGAGGAGGACACATGATTTCTC 960
 Qy 321 ProIleValLeuGlnTyrLeuCysProValTyrIleSerPhePheGlyLeuGlyAlaVal 340
 Db 961 CCGATCGTCTCGAGTACCTCTCTGCTGTATACATCTCTCTCTCTGGGTGGTGGTGT 1020
 Qy 341 SerAlaAlaValMetSerSerAlaAspSerSerIleLeuSerAlaSerMetPheAla 360
 Db 1021 TCAGCTGTGTATGCTCTCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 Qy 361 ArgAsnIleTyrGlnLeuSerPheArgGlnAsnAlaSerAspLysGluIleValTrpVal 380
 Db 1081 CGGAATATCTACAGCTTTCTCTTCAGACAAATTCATTCAGACAGGAAATTTGTGGGTCT 1140
 Qy 381 MetArgIleThrValLeuValPheGlyAlaSerAlaThrAlaMetAlaLeuLeuThrLys 400
 Db 1141 ATGAGGATCATCTGTCTGTGTGTCGGAGCATCTGCAACAGCCATGGCTTGTGTCGAGAG 1200
 Qy 401 ThrValTyrGlyLeuTrpTyrLeuSerSerAspLeuValTyrIleIleIlePheProGln 420
 Db 1201 ACTGTGTATGGGCTCTGTACCTGAGCTCTGACCTGTCTGCTTACATCATCTTCCACAG 1260

Qy 421 LeuLeuCysValLeuPheIleLysGlyThrAsnThrTyrGlyAlaValAlaGlyTyrIle 440
 Db 1261 CTGCTCTGTGTACTCTTTCATCAAGGAACCAACACATATATGGGCGAGTCTGTGTATATT 1320
 Qy 441 PheGlyLeuPheIleLeuArgIleThrGlyGlyGluProTyrLeuTyrLeuGlnProLeuIle 460
 Db 1321 TTTTGACTATTTCTCGAATTTACTTGGAGGAGAGCCATATCTTACTTTGAGCCCTTAATC 1380
 Qy 461 PheTyrProGlyTyrTyrSerAspLysAsnGlyIleTyrAsnGlnArgPheProPheLys 480
 Db 1381 TTCTACCTGGTTATTACTCTGACAAGAATGGTATATACAAATCAGAGGTTCCCATTTAAA 1440
 Qy 481 ThrLeuSerMetValThrSerPhePheThrAsnIleCysValSerTyrLeuAlaLysTyr 500
 Db 1441 ACTCTCTCCATGGTTACTCTTCTTACCACAAATTTGTGTCTTCTTATCTAGCCAAAGTAT 1500
 Qy 501 LeuPheGluSerGlyThrLeuProProLysLeuAspValPheAspAlaValAlaAlaArg 520
 Db 1501 CTATTTGAAAGTGGAACTTGCCTCCAAAATTAGATGTATTTGATGCTGTGTGCGCAAGG 1560
 Qy 521 HisSerGluGluAsnMetAspLysThrIleLeuValArgAsnGluAsnIleLysLeuAsn 540
 Db 1561 CACAGTGAGAGACATCGACAGACCATCTTAGTCAGAAATGAAATATCAAAATTAAT 1620
 Qy 541 GluLeuAlaProValLysProArgGlnSerLeuThrLeuSerSerThrPheThrAsnLys 560
 Db 1621 GAACCTTGACCTGTGAAACCTCGGACAGCCCTAACCCCTCAGTTCAACTTTTCCCAATAAG 1680
 Qy 561 GluAlaLeuLeuAspValAspSerSerProGluGlySerGlyThrGluAspAsnLeuGln 580
 Db 1681 GAGGCCCTCTCTGTATTTGATTTCCAGTCCGAGGGGTCTGGAGCTGAAGATAACTTACAA 1740

RESULT 4

E49872 1743 bp DNA linear PAT 27-AUG-2002
 LOCUS High-affinity choline transporter.
 DEFINITION E49872
 ACCESSION E49872
 VERSION E49872.1 GI:22554903
 KEYWORDS JP 2001136976-A/4.
 SOURCE Mus sp.
 ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1743)
 AUTHORS Haga, T. and Okuda, T.
 TITLE High-affinity choline transporter
 JOURNAL Patent: JP 2001136976-A 4 22-MAY-2001;
 SCIENCE & TECH AGENCY

COMMENT
 OS Mus sp. (mouse)
 PN JP 2001136976-A/4
 PD 22-MAY-2001
 PF 27-DEC-1999 JP 1999368991
 PI TATSUYA HAGA, TAKASHI OKUDA
 PC C12N15/09, A01K67/027, A61K38/00, C07K14/47, C07K16/18, C07K19/00,
 PC C12N5/10,
 PC C12P21/02, C12P21/08, C12Q1/00, C12N15/00, A61K37/02, C12N5/00 CC
 PH Key Location/Qualifiers
 FT CDS (1)..(1743).

FEATURES

source
 1..1743
 /organism="Mus sp."
 /mol_type="genomic DNA"
 /db_xref="taxon:10095"

ORIGIN

Alignment Scores:
 Pred. No.: 0 Length: 1743
 Score: 2968.00 Matches: 576
 Percent Similarity: 99.5% Conservative: 1
 Best Local Similarity: 99.3% Mismatches: 3
 Query Match: 99.2% Indels: 0